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The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 2.

## EXAMPLE 5

Construction of an over-expression vector with a fruit enhanced promoter.

The complete sequence of a ripening -related cDNA containing a full open-reading frame is inserted into the vectors described in EXAMPLE 3.

## EXAMPLE 6

Generation of transformed Musa plants

Transformed Musa plants containing the vectors are produced by the method described in Sagi et al. (1995) Biotechnology. Vol. 13 pp 481-485. Regenerated transformed plants are identified by their ability to grow on hygromycin and grown to maturity. Ripening fruit are analysed for a modulation in their ripening related or senescence characteristics.

Other suitable transformation methods for banana are described in Sagi et al. (1994) Plant Cell Reports. Vol. 13. pp 262-266. and May et al. (1995) Biotechnology. Vol. 13 pp 486-492.

**TABLE 1**

| Sequence Identity | Group | Clone no. | Size Kb | Published Sequence gene Identity | % Identity | Sequence Bp | Published Sequences |
|---|---|---|---|---|---|---|---|
| SEQ-ID-NO-1 | Pulp Upregulated | U-U9 | 1 | Isoflavone Reductase | 61.6 | 714 | Potato (Solanum tuberosum), X92075 |
| SEQ-ID-NO-2 | Pulp Upregulated | U-U17 | 1 | Isoflavone Reductase | 62.9 | 770 | Potato (Solanum tuberosum), X92075 |
| SEQ-ID-NO-3 | Pulp Upregulated | U-U66 | 1.1 | Isoflavonoid Reductase | 60.0 | 722 | Arabidopsis thailiana, Z49777 |
| SEQ-ID-NO-4 | Pulp Upregulated | U-U104 | 1 | Isoflavonoid Reductase | 60.6 | 696 | Arabidopsis thailiana Z49777 |
| SEQ-ID-NO-5 | Pulp Upregulated | U-U13 | 1.1 | Beta-1,3-Glucanase | 58.5 | 585 | Soybean (Glycine max), A26451 |
| SEQ-ID-NO-6 | Pulp Upregulated | U-U136 | 1.3 | Beta-1,3-Glucanase | 59.8 | 800 | Barley (Hordeum vulgare), M91814 |
| SEQ-ID-NO-7 | Pulp Upregulated | U-U21 | 1.8 | Transcriptional Activator | 54.3 | 311 | Zea mays, L13454 |

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| Sequence Identity | Group | Clone no. | Size Kb | Published Sequence gene Identity | % Identity | Sequence Bp | Published Sequences |
|---|---|---|---|---|---|---|---|
| SEQ-ID-NO-8 | Pulp Upregulated | U-U31 | 0.55 | S-adenosylhomocysteine Hydrolase | 67.0 | 467 | Orchid (*Phalaenopsis sp.*), X79905 |
| SEQ-ID-NO-9 | Pulp Upregulated | U-U131 | 1.8 | S-adenosyl L-homocysteine Hydrolase | 79.8 | 699 | Wheat (*Triticum aestivum*), L11872 |
| SEQ-ID-NO-10 | Pulp Upregulated | U-U32 | 0.8 | Beta-amylase | 54.7 | 854 | *Zea mays*, Z25871 |
| SEQ-ID-NO-11 | Pulp Upregulated | U-U55 | 0.8 | O-methyl transferases | 60.1 | 223 | *Zea mays*, L14063 |
| SEQ-ID-NO-12 | Pulp Upregulated | U-U72 | 0.8 | O-methyl transferase | 60.6 | 226 | *Zea mays*, L14063 |
| SEQ-ID-NO-13 | Pulp Upregulated | U-U68 | 1.8 | Pectate Lyase | 57.9 | 394 | *Lilium longiflorum*, Z17328 |
| SEQ-ID-NO-14 | Pulp Upregulated | U-U69 | 1.7 | Pectate Lyase | 66.1 | 516 | *Zea mays*, L20140 |
| SEQ-ID-NO-15 | Pulp Upregulated | U-U84 | 1.1 | Pectate Lyase | 65.8 | 736 | *Lycopersicon esculentum*, X55193 |
| SEQ-ID-NO-16 | Pulp Upregulated | U-U89 | 1.6 | Pectate Lyase | 54.8 | 354 | *Nicotiana tabacum*, X67158 |